

RAW SEQUENCE LISTING

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Application Serial Number: 10/619,992 A
Source: IFW16
Date Processed by STIC: 12/06/2005

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IFW16

RAW SEQUENCE LISTING DATE: 12/06/2005
PATENT APPLICATION: US/10/619,992A TIME: 13:09:50

Input Set : D:\00-617-F.ST25.txt
Output Set: N:\CRF4\12062005\J619992A.raw

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3 <110> APPLICANT: Oregon Health & Science University
4     Hefeneider, Steven
5     Bennett, Robert
6     Seiss, Donald
7     Merkins, Louise
9 <120> TITLE OF INVENTION: Mammalian Cell Surface DNA Receptor
11 <130> FILE REFERENCE: 00-617-F
13 <140> CURRENT APPLICATION NUMBER: US 10/619992A
14 <141> CURRENT FILING DATE: 2003-07-15
16 <150> PRIOR APPLICATION NUMBER: 09/921,099
17 <151> PRIOR FILING DATE: 2001-08-01
19 <160> NUMBER OF SEQ ID NOS: 21
21 <170> SOFTWARE: PatentIn version 3.3
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 4351
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (602)..(4174)
33 <400> SEQUENCE: 1
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38 tattatgttt tgggttactg gtatccaag ggaaacactt tttaaacaaa caaaacaaaa    180
40 aaaccggcca gcagtc当地 gtaatttgg ttcctaaaaa tggatatgg aaagttattt    240
42 tgcttgggg atgtggcgt tgagaaaaat acataaaagc tttatgtttt attatgttag    300
44 caaccaatat aaatacagtt tagtgaaag gaacactatt aaggtattgt ttccaggcag    360
46 aatttcagaa atgtattaa ttccagaaat aggtttta aaaaagacat ccaaaggta      420
48 taaaattatt tagaagtatt tttaggtctga agctgtataa gttgacttaa gcaattaact    480
50 cttcaaaggta gaatgtgaa tatgtggta attcatactt ttgtccattt ctatgttaca    540
52 aaacactaca cagcaaaaata atgatctgct agactgctaa cccgagcatc cagttccac    600
54 a atg cct gtg cag gca gct caa tgg aca gaa ttt ctg tcc tgt cca atc    649
55 Met Pro Val Gln Ala Ala Gln Trp Thr Glu Phe Leu Ser Cys Pro Ile
56   1           5           10          15
58 tgc tat aat gaa ttt gat gag aat gtg cac aaa ccc atc agt tta ggt      697
59 Cys Tyr Asn Glu Phe Asp Glu Asn Val His Lys Pro Ile Ser Leu Gly
60       20           25           30
62 tgt tca cac act gtt tgc aag acc tgc ttg aat aaa ctt cat cga aaa      745
63 Cys Ser His Thr Val Cys Lys Thr Cys Leu Asn Lys Leu His Arg Lys
64       35           40           45
66 gct tgt cct ttt gac cag act gcc atc aac aca gat att gat gta ctt      793
67 Ala Cys Pro Phe Asp Gln Thr Ala Ile Asn Thr Asp Ile Asp Val Leu
68       50           55           60

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71	Pro	Val	Asn	Phe	Ala	Leu	Leu	Gln	Leu	Val	Gly	Ala	Gln	Val	Pro	Asp		
72	65					70				75						80		
74	cat	cag	tca	att	aag	tta	agt	aat	cta	ggt	gag	aat	aaa	cac	tat	gag		889
75	His	Gln	Ser	Ile	Lys	Leu	Ser	Asn	Leu	Gly	Glu	Asn	Lys	His	Tyr	Glu		
76						85				90						95		
78	gtt	gca	aag	aaa	tgc	gtt	gag	gat	ttg	gca	ctc	tac	tta	aaa	cca	cta		937
79	Val	Ala	Lys	Lys	Cys	Val	Glu	Asp	Leu	Ala	Leu	Tyr	Leu	Lys	Pro	Leu		
80						100				105						110		
82	agt	gga	ggg	aaa	ggg	gtt	gta	gct	agc	ttg	aac	cag	agt	gca	ctg	agc	cgt	985
83	Ser	Gly	Gly	Lys	Gly	Val	Ala	Ser	Leu	Asn	Gln	Ser	Ala	Leu	Ser	Arg		
84						115				120						125		
86	cca	atg	caa	agg	aaa	ctg	gtg	aca	ctt	gta	aac	tgt	caa	ctg	gtg	gag		1033
87	Pro	Met	Gln	Arg	Lys	Leu	Val	Thr	Leu	Val	Asn	Cys	Gln	Leu	Val	Glu		
88						130				135						140		
90	gaa	gaa	ggg	ggg	gtt	gta	aga	gcc	atg	cga	gca	gct	cgt	tcc	ctt	gga	gaa	1081
91	Glu	Glu	Gly	Arg	Val	Arg	Ala	Met	Arg	Ala	Ala	Arg	Ser	Leu	Gly	Glu		
92	145					150				155						160		
94	aga	act	gta	aca	gaa	ctg	ata	tta	cag	cac	cag	aac	cct	cag	cag	ttg		1129
95	Arg	Thr	Val	Thr	Glu	Leu	Ile	Leu	Gln	His	Gln	Asn	Pro	Gln	Gln	Leu		
96						165				170						175		
98	tct	gcc	aat	cta	tgg	gcc	gct	gtc	agg	gct	cga	gga	tgc	cag	ttt	tta		1177
99	Ser	Ala	Asn	Leu	Trp	Ala	Ala	Val	Arg	Ala	Arg	Gly	Cys	Gln	Phe	Leu		
100						180				185						190		
102	ggg	cca	gct	atg	caa	gaa	gag	gcc	ttg	aag	ctg	gtg	tta	ctg	gca	tta		1225
103	Gly	Pro	Ala	Met	Gln	Glu	Glu	Ala	Leu	Lys	Leu	Val	Leu	Leu	Ala	Leu		
104						195				200						205		
106	gaa	gat	ggg	tct	gcc	ctc	tca	agg	aaa	gtt	ctg	gta	ctt	ttt	gtt	gtg		1273
107	Glu	Asp	Gly	Ser	Ala	Leu	Ser	Arg	Lys	Val	Leu	Val	Leu	Phe	Val	Val		
108						210				215						220		
110	cag	aga	cta	gaa	cca	aga	ttt	cct	cag	gca	tca	aaa	aca	agt	att	ggg		1321
111	Gln	Arg	Leu	Glu	Pro	Arg	Phe	Pro	Gln	Ala	Ser	Lys	Thr	Ser	Ile	Gly		
112	225					230				235						240		
114	cat	gtt	gtg	caa	cta	ctg	tat	cga	gct	tct	tgt	ttt	aag	gtt	acc	aaa		1369
115	His	Val	Val	Gln	Leu	Leu	Tyr	Arg	Ala	Ser	Cys	Phe	Lys	Val	Thr	Lys		
116						245				250						255		
118	aga	gat	gaa	gac	tct	tcc	cta	atg	cag	ctg	aag	gag	gaa	ttt	cgg	agt		1417
119	Arg	Asp	Glu	Asp	Ser	Ser	Leu	Met	Gln	Leu	Lys	Glu	Glu	Phe	Arg	Ser		
120						260				265						270		
122	tat	gaa	gca	tta	cgc	aga	gaa	cat	gat	gcc	caa	att	gtt	cat	att	gcc		1465
123	Tyr	Glu	Ala	Leu	Arg	Arg	Glu	His	Asp	Ala	Gln	Ile	Val	His	Ile	Ala		
124						275				280						285		
126	atg	gaa	gca	gga	ctc	cgt	att	tca	cct	gaa	cag	tgg	tcc	tct	ctt	ttg		1513
127	Met	Glu	Ala	Gly	Leu	Arg	Ile	Ser	Pro	Glu	Gln	Trp	Ser	Ser	Leu	Leu		
128						290				295						300		
130	tat	ggg	gtt	gat	ttg	gct	cat	aaa	tca	cac	atg	cag	tct	atc	att	gat	aag	1561
131	Tyr	Gly	Asp	Glu	Leu	Ala	His	Lys	Ser	His	Met	Gln	Ser	Ile	Ile	Asp	Lys	
132	305					310				315						320		
134	cta	cag	tct	cca	gag	tca	ttt	gca	aag	agt	gtc	cag	gaa	ttg	aca	att		1609

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139 Val Leu Gln Arg Thr Gly Asp Pro Ala Asn Leu Asn Arg Leu Arg Pro
140          340          345          350
142 cat tta gag ctt ctt gca aac ata gac cct aat cca gac gct gtt tca      1705
143 His Leu Glu Leu Ala Asn Ile Asp Pro Asn Pro Asp Ala Val Ser
144          355          360          365
146 cca act tgg gag cag ctg gaa aat gca atg gta gct gtt aaa aca gta      1753
147 Pro Thr Trp Glu Gln Leu Glu Asn Ala Met Val Ala Val Lys Thr Val
148          370          375          380
150 gtt cat ggc ctt gtg gac ttc ata caa aat tat agt aga aaa ggc cat      1801
151 Val His Gly Leu Val Asp Phe Ile Gln Asn Tyr Ser Arg Lys Gly His
152 385          390          395          400
154 gag acc cct cag cag cca aac agc aaa tac aag act agc atg tgc      1849
155 Glu Thr Pro Gln Pro Gln Pro Asn Ser Lys Tyr Lys Thr Ser Met Cys
156          405          410          415
158 cga gat ttg cga cag cag ggg ggt tgt cca cga gga aca aat tgt aca      1897
159 Arg Asp Leu Arg Gln Gln Gly Gly Cys Pro Arg Gly Thr Asn Cys Thr
160          420          425          430
162 ttt gcc cat tct cag gaa gag ctt gaa aag tat cga tta agg aac aaa      1945
163 Phe Ala His Ser Gln Glu Leu Glu Lys Tyr Arg Leu Arg Asn Lys
164          435          440          445
166 aag atc aat gcc act gta aga acg ttt cct ctt cta aat aaa gtt ggt      1993
167 Lys Ile Asn Ala Thr Val Arg Thr Phe Pro Leu Leu Asn Lys Val Gly
168          450          455          460
170 gta aac aac act gtc aca acc aca gcc gga aat gtc att tct gtc ata      2041
171 Val Asn Asn Thr Val Thr Thr Ala Gly Asn Val Ile Ser Val Ile
172 465          470          475          480
174 gga agt act gaa aca aca ggg aaa att gtt cca agt aca aac gga att      2089
175 Gly Ser Thr Glu Thr Thr Gly Lys Ile Val Pro Ser Thr Asn Gly Ile
176          485          490          495
178 tca aat gca gaa aac agt gtt tcc cag cta atc tca cgt agt act gac      2137
179 Ser Asn Ala Glu Asn Ser Val Ser Gln Leu Ile Ser Arg Ser Thr Asp
180          500          505          510
182 agt acc tta aga gct ctg gag acc gtg aag aaa gtg gga aag gtt ggc      2185
183 Ser Thr Leu Arg Ala Leu Glu Thr Val Lys Lys Val Gly Lys Val Gly
184          515          520          525
186 gct aat ggt cag aat gct gct ggg ccc tct gca gat tct gta act gaa      2233
187 Ala Asn Gly Gln Asn Ala Ala Gly Pro Ser Ala Asp Ser Val Thr Glu
188          530          535          540
190 aat aaa att ggt tct cca ccc aag act cct gta agt aat gta gca gct      2281
191 Asn Lys Ile Gly Ser Pro Pro Lys Thr Pro Val Ser Asn Val Ala Ala
192 545          550          555          560
194 acc tca gct ggg ccc tct aat gtt gga aca gag ctg aat tct gtg cct      2329
195 Thr Ser Ala Gly Pro Ser Asn Val Gly Thr Glu Leu Asn Ser Val Pro
196          565          570          575
198 caa aaa tcc agc cca ttt cta act aga gta cca gta tat cct ccg cat      2377
199 Gln Lys Ser Ser Pro Phe Leu Thr Arg Val Pro Val Tyr Pro Pro His
  
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203	Ser Glu Asn Ile Gln Tyr Phe Gln Asp Pro Arg Thr Gln Ile Pro Phe			
204	595	600	605	
206	gaa gtc cca cag tac cca cag aca gga tac tat cca cca cct cca acg			2473
207	Glu Val Pro Gln Tyr Pro Gln Thr Gly Tyr Tyr Pro Pro Pro Pro Thr			
208	610	615	620	
210	gta cca gct ggt gtg gct ccc tgt gtt cct cgc ttt gtg agg tcc aat			2521
211	Val Pro Ala Gly Val Ala Pro Cys Val Pro Arg Phe Val Arg Ser Asn			
212	625	630	635	640
214	aac gtt cca gag tcc tcc ctc cca cct gct tcc atg cca tat gcc gat			2569
215	Asn Val Pro Glu Ser Ser Leu Pro Pro Ala Ser Met Pro Tyr Ala Asp			
216	645	650	655	
218	cat tac agt aca ttt tcc cct cga gat cga atg aat tct tct cct tac			2617
219	His Tyr Ser Thr Phe Ser Pro Arg Asp Arg Met Asn Ser Ser Pro Tyr			
220	660	665	670	
222	cag cct cct ccg cag ccg tat gga cca gtt cct cca gta cct tct			2665
223	Gln Pro Pro Pro Gln Pro Tyr Gly Pro Val Pro Pro Val Pro Ser			
224	675	680	685	
226	gga atg tat gct cct gtg tac gac agc agg cgc atc tgg cgc cca cct			2713
227	Gly Met Tyr Ala Pro Val Tyr Asp Ser Arg Arg Ile Trp Arg Pro Pro			
228	690	695	700	
230	atg tac caa cga gat gac att att aga agc aat tct tta cct cca atg			2761
231	Met Tyr Gln Arg Asp Asp Ile Ile Arg Ser Asn Ser Leu Pro Pro Met			
232	705	710	715	720
234	gat gtg atg cac tca tct gtc tat cag aca tct ttg cgg gaa aga tat			2809
235	Asp Val Met His Ser Ser Val Tyr Gln Thr Ser Leu Arg Glu Arg Tyr			
236	725	730	735	
238	aac tca tta gat gga tat tat tcg gtg gct tgt cag cca cca agt gag			2857
239	Asn Ser Leu Asp Gly Tyr Tyr Ser Val Ala Cys Gln Pro Pro Ser Glu			
240	740	745	750	
242	cca agg aca act gtg cct tta cca agg gaa cct tgt ggt cat ttg aag			2905
243	Pro Arg Thr Thr Val Pro Leu Pro Arg Glu Pro Cys Gly His Leu Lys			
244	755	760	765	
246	acc agt tgc gag gag cag ata aga aga aag cca gat cag tgg gca cag			2953
247	Thr Ser Cys Glu Glu Gln Ile Arg Arg Lys Pro Asp Gln Trp Ala Gln			
248	770	775	780	
250	tac cac act cag aaa gca cct ctt gtc tct tca act ctt cct gtg gca			3001
251	Tyr His Thr Gln Lys Ala Pro Leu Val Ser Ser Thr Leu Pro Val Ala			
252	785	790	795	800
254	aca cag tca cca aca cca cct tct cct ctg ttc agt gta gac ttt cgt			3049
255	Thr Gln Ser Pro Thr Pro Pro Ser Pro Leu Phe Ser Val Asp Phe Arg			
256	805	810	815	
258	gcg gat ttc tca gag agt gtg agt ggt aca aaa ttt gaa gaa gat cat			3097
259	Ala Asp Phe Ser Glu Ser Val Ser Gly Thr Lys Phe Glu Glu Asp His			
260	820	825	830	
262	ctt tcc cat tat tct ccc tgg tct tgt ggc acc ata ggc tcc tgt ata			3145
263	Leu Ser His Tyr Ser Pro Trp Ser Cys Gly Thr Ile Gly Ser Cys Ile			
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266 aat gcc att gat tca gag ccc aaa gat gtc att gct aat tca aat gct	3193
267 Asn Ala Ile Asp Ser Glu Pro Lys Asp Val Ile Ala Asn Ser Asn Ala	
268 850 855 860	
270 gtg tta atg gac ctg gac agt ggt gat gtt aag aga aga gta cat tta	3241
271 Val Leu Met Asp Leu Asp Ser Gly Asp Val Lys Arg Arg Val His Leu	
272 865 870 875 880	
274 ttt gaa acc cag aga agg aca aaa gaa gaa gat cca ata att ccc ttt	3289
275 Phe Glu Thr Gln Arg Arg Thr Lys Glu Glu Asp Pro Ile Ile Pro Phe	
276 885 890 895	
278 agt gat gga ccc atc atc tca aaa tgg ggt gcg att tcc aga tct tcc	3337
279 Ser Asp Gly Pro Ile Ile Ser Lys Trp Gly Ala Ile Ser Arg Ser Ser	
280 900 905 910	
282 cgt aca ggt tac cat acc aca gat cct gtc cag gcc act gct tcc caa	3385
283 Arg Thr Gly Tyr His Thr Asp Pro Val Gln Ala Thr Ala Ser Gln	
284 915 920 925	
286 gga agt gcg act aag ccc atc agt gta tca gat tat gtc cct tat gtc	3433
287 Gly Ser Ala Thr Lys Pro Ile Ser Val Ser Asp Tyr Val Pro Tyr Val	
288 930 935 940	
290 aat gct gtt gat tca agg tgg agt tca tat ggc aac gag gcc aca tca	3481
291 Asn Ala Val Asp Ser Arg Trp Ser Ser Tyr Gly Asn Glu Ala Thr Ser	
292 945 950 955 960	
294 tca gca cac tat gtt gaa agg gac aga ttc att gtt act gat tta tct	3529
295 Ser Ala His Tyr Val Glu Arg Asp Arg Phe Ile Val Thr Asp Leu Ser	
296 965 970 975	
298 ggt cat aga aag cat tcc agt act ggg gac ctt ttg agc ctt gaa ctt	3577
299 Gly His Arg Lys His Ser Ser Thr Gly Asp Leu Leu Ser Leu Glu Leu	
300 980 985 990	
302 cag cag gcc aag agc aac tca tta ctt ctt cag aga gag gcc aat gct	3625
303 Gln Gln Ala Lys Ser Asn Ser Leu Leu Leu Gln Arg Glu Ala Asn Ala	
304 995 1000 1005	
306 ttg gcc atg caa cag aag tgg aat tcc ctg gat gaa ggc cgt cac	3670
307 Leu Ala Met Gln Gln Lys Trp Asn Ser Leu Asp Glu Gly Arg His	
308 1010 1015 1020	
310 ctt acc tta aac ctt tta agc aag gaa att gaa cta aga aat gga	3715
311 Leu Thr Leu Asn Leu Leu Ser Lys Glu Ile Glu Leu Arg Asn Gly	
312 1025 1030 1035	
314 gag tta cag agt gat tat aca gaa gat gca aca gat act aaa cct	3760
315 Glu Leu Gln Ser Asp Tyr Thr Glu Asp Ala Thr Asp Thr Lys Pro	
316 1040 1045 1050	
318 gat agg gat atc gag tta gag ctt tca gca ctt gat act gat gaa	3805
319 Asp Arg Asp Ile Glu Leu Glu Leu Ser Ala Leu Asp Thr Asp Glu	
320 1055 1060 1065	
322 cct gat gga caa agt gaa cca att gaa gag atc ttg gac ata cag	3850
323 Pro Asp Gly Gln Ser Glu Pro Ile Glu Glu Ile Leu Asp Ile Gln	
324 1070 1075 1080	
326 ctt ggt atc agt tct caa aat gat cag ttg cta aat gga atg gca	3895
327 Leu Gly Ile Ser Ser Gln Asn Asp Gln Leu Leu Asn Gly Met Ala	
328 1085 1090 1095	
330 gtg gaa aat ggg cat cca gta cag cag cac caa aag gag cca cca	3940

VERIFICATION SUMMARY

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